

LISTING OF CLAIMS

This Listing of Claims will replace all prior versions, and listings, of claims in the application:

Claims 1-19 (canceled)

20. (withdrawn): A library of nucleic acid sequences consisting essentially of nucleic acid sequences having at least about 80% protein sequence identity to a nucleic acid sequence selected from the group consisting of the *Staphylococcus aureus* open reading frames(ORFs) listed in Table1, wherein said library of nucleic acid sequences is employed to identify essential genes in *Staphylococcus*.

21. (withdrawn): A map of at least about 500-1500 transposon insertions in the genome of *Staphylococcus aureus*, wherein said map is useful for identifying genes that are essential for survival of said *Staphylococcus aureus*.

Claims 22-37 (canceled)

38. (withdrawn): The nucleic acid library of claim 20, wherein said map is in electronic form.

39. (withdrawn): The library of claim 38, wherein said electronic form is selected from the group consisting of magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media

such as RAM and ROM; hybrids of these categories such as magnetic/optical storage media; computer readable forms such as a word processing text file, database format, searchable files, executable files and search program software.

40. (withdrawn): The transposon insertion map of claim 21, wherein said map is in electronic form.

41. (withdrawn): The map of claim 38, wherein said electronic form is selected from the group consisting of magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; hybrids of these categories such as magnetic/optical storage media; computer readable forms such as a word processing text file, database format, searchable files, executable files and search program software.

42. (currently amended): A method for identifying a library of putative essential or important genes using a High Throughput Transposon Insertion Map (HTTIM) database, comprising:

a) mutagenizing a *Staphylococcus* genome with a transposon such that individual cells, each containing at least one transposon insertion site that received a transposon insertion, are isolated;

b) ~~collecting and mapping polynucleotide sequences of~~ sequencing said at least one transposon insertion site in each individual cell so as to form a database of ~~said~~ polynucleotide sequences of transposon insertion sites, or an HTTIM database;

c) comparing said polynucleotide sequences of transposon insertion sites with the *Staphylococcus* genomic sequence to identify open reading frames in said *Staphylococcus* genomic sequence that are not disrupted by a transposon insertion; and

d) forming a library of putative essential or important genes from said open reading frames in said *Staphylococcus* genomic sequence that are not disrupted by a transposon insertion.

43. (previously presented): The method of claim 42, wherein said genomic sequence is from *S. aureus*.

44. (original): The method of claim 42, wherein said transposon inserts randomly into the target genome.

45. (previously presented): The method of claim 42, wherein said HTTIM database comprises polynucleotide sequences of at least about 3,000 to 6,000 transposon insertion sites.

46. (previously presented): The method of claim 45, wherein said HTTIM database comprises polynucleotide sequences of at least about 4,000 to 5,000 transposon insertion sites.

47. (original): The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 500 to 1850 genes.

48. (original): The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 1000 to 1400 genes.

49. (original): The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 600-625 genes.

50. (original): The library of putative essential or important genes identified by the method of claim 42, wherein said library comprises at most about 530-543 genes.

51. (original): The method of claim 42, further comprising a statistical calculation for identifying putative essential or important genes.

52. (previously presented): The method of claim 51, wherein the statistical calculation utilizes a Bayesian statistical model.

53. (original): The method of claim 42, further comprising a physical mutagenesis experiment in order to verify essential or important genes.

54. (original): The method of claim 53, wherein said physical mutagenesis comprises knocking out a putative essential or important gene or creating a promoter swap mutant.

55. (original): An essential or important gene identified by the method of claim 53.

56. (withdrawn): An antibacterial agent that targets the gene of claim 55, or the gene product encoded by said gene.

Claim 57 (canceled)